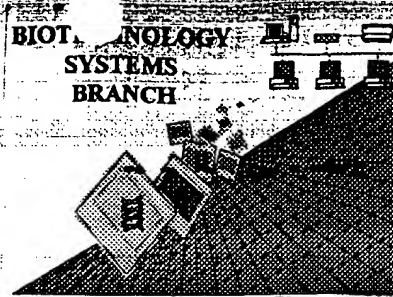


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/733,773

Source: OIA

Date Processed by STIC: 12/21/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/733,773A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid "bug" sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence: (OLD RULES) (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence. (NEW RULES) <210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES) Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

#2 OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/733,773

DATE: 12/21/2000
 TIME: 10:13:10

Input Set : A:\SALK2410.ST25.txt
 Output Set: N:\CRF3\12212000\I733773.raw

Does Not Comply
 Corrected Diskette Needed

ppr 2-3,5

OK

3 <110> APPLICANT: The Salk Institute For Biological Studies
 4 NOEL, Joseph
 5 VERDECIAN, Mark
 7 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF WW DOMAINS AND METHODS AND USE THEREOF
 9 <130> FILE REFERENCE: SALK2410
 11 <140> CURRENT APPLICATION NUMBER: US/09/733,773
 12 <141> CURRENT FILING DATE: 2000-12-08
 14 <160> NUMBER OF SEQ ID NOS: 32
 16 <170> SOFTWARE: PatentIn version 3.0
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 163
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: PEPTIDE
 25 <222> LOCATION: (1)..(163)
 26 <223> OTHER INFORMATION: Pin1
 29 <400> SEQUENCE: 1
 31 Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
 32 1 5 10 15
 34 Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
 35 20 25 30
 37 Glu Trp Glu Arg Pro Ser Gly Asn Ser Ser Ser Gly Gly Lys Asn Gly
 38 35 40 45
 40 Glu Gly Glu Pro Ala Arg Val Arg Cys Ser His Leu Val Lys His
 41 50 55 60
 43 Ser Gln Ser Arg Arg Pro Ser Ser Trp Arg Gln Glu Lys Ile Thr Arg
 44 65 70 75 80
 46 Thr Lys Glu Glu Ala Leu Glu Leu Ile Asn Gly Tyr Ile Gln Lys Ile
 47 85 90 95
 49 Lys Ser Gly Glu Glu Asp Phe Glu Ser Leu Ala Ser Gln Phe Ser Asp
 50 100 105 110
 52 Cys Ser Ser Ala Lys Ala Arg Gly Asp Leu Gly Ala Phe Ser Arg Gly
 53 115 120 125
 55 Glu Met Gln Lys Pro Phe Glu Asp Ala Ser Phe Ala Leu Arg Thr Gly
 56 130 135 140
 58 Glu Met Ser Gly Pro Val Phe Thr Asp Ser Gly Ile His Ile Ile Leu
 59 145 150 155 160
 61 Arg Thr Glu
 64 <210> SEQ ID NO: 2
 65 <211> LENGTH: 38
 66 <212> TYPE: PRT
 67 <213> ORGANISM: Homo sapiens
 69 <220> FEATURE:
 70 <221> NAME/KEY: DOMAIN
 71 <222> LOCATION: (1)..(38)
 72 <223> OTHER INFORMATION: Ww Domain of Pin1

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/733,773
 DATE: 12/21/2000
 TIME: 10:13:40
 Input Set : A:\SALK2410.ST25.txt
 Output Set: N:\CRF3\12212000\I733773.raw

75 <400> SEQUENCE: 2
 77 Met Ala Asp Glu Glu Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser
 78 1 5 10 15
 80 Arg Ser Ser Gly Arg Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser
 81 20 25 30
 83 Gln Trp Glu Arg Pro Ser
 84 35
 86 <210> SEQ ID NO: 3
 87 <211> LENGTH: 7
 88 <212> TYPE: PRT
 89 <213> ORGANISM: Homo sapiens
 91 <220> FEATURE:
 92 <221> NAME/KEY: MOD_RES
 93 <222> LOCATION: (2)..(2)
 94 <223> OTHER INFORMATION: PHOSPHORYLATION
 97 <220> FEATURE:
 98 <221> NAME/KEY: MOD_RES
 99 <222> LOCATION: (5)..(5)
 100 <223> OTHER INFORMATION: PHOSPHORYLATION
 103 <400> SEQUENCE: 3
 105 Tyr Ser Pro Thr Ser Pro Ser
 106 1 5
 108 <210> SEQ ID NO: 4
 109 <211> LENGTH: 9
 110 <212> TYPE: PRT
 111 <213> ORGANISM: ARTIFICIAL
 113 <220> FEATURE:
 114 <223> OTHER INFORMATION: PEPTIDE
 116 <220> FEATURE:
 117 <221> NAME/KEY: VARIANT
 118 <222> LOCATION: (6)..(6)
 119 <223> OTHER INFORMATION: Xaa is any amino acid (Pro in Figure 4a & 4b)
 122 <400> SEQUENCE: 4
 124 Gly Thr Pro Pro Pro Xaa Tyr Thr Val
 125 1 5
 127 <210> SEQ ID NO: 5
 128 <211> LENGTH: 8
 129 <212> TYPE: PRT
 130 <213> ORGANISM: ARTIFICIAL
 132 <220> FEATURE:
 133 <223> OTHER INFORMATION: Peptide
 135 <400> SEQUENCE: 5
 137 Trp Phe Tyr Ser Pro Phe Leu Glu
 138 1 5
 140 <210> SEQ ID NO: 6
 141 <211> LENGTH: 8
 142 <212> TYPE: PRT
 143 <213> ORGANISM: ARTIFICIAL
 145 <220> FEATURE:

*invalid response - give source of genetic material -
 (see circled portion of
 item 12 on
 Eva summary
 sheet)*

OK

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/733,773

DATE: 12/21/2000
TIME: 10:13:40

Input Set : A:\SALK2410.ST25.txt
Output Set: N:\CRF3\12212000\I733773.raw

146 <223> OTHER INFORMATION: Peptide
148 <220> FEATURE:
149 <221> NAME/KEY: MOD_RES
150 <222> LOCATION: (1)..(4)
151 <223> OTHER INFORMATION: PHOSPHORYLATION
154 <400> SEQUENCE: 6
156 Trp Phe Tyr Ser Pro Phe Leu Glu
157 1 5
159 <210> SEQ ID NO: 7
160 <211> LENGTH: 6
161 <212> TYPE: PRT
162 <213> ORGANISM: Homo sapiens
164 <220> FEATURE:
165 <221> NAME/KEY: MOD_RES
166 <222> LOCATION: (4)..(4)
167 <223> OTHER INFORMATION: PHOSPHORYLATION
170 <400> SEQUENCE: 7
172 Val Pro Arg Thr Pro Val
173 1 5
175 <210> SEQ ID NO: 8
176 <211> LENGTH: 6
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <220> FEATURE:
181 <221> NAME/KEY: MOD_RES
182 <222> LOCATION: (4)..(4)
183 <223> OTHER INFORMATION: PHOSPHORYLATION
186 <400> SEQUENCE: 8
188 Tyr Leu Gly Ser Pro Ile
189 1 5
191 <210> SEQ ID NO: 9
192 <211> LENGTH: 6
193 <212> TYPE: PRT
194 <213> ORGANISM: Homo sapiens
196 <220> FEATURE:
197 <221> NAME/KEY: MOD_RES
198 <222> LOCATION: (1)..(4)
199 <223> OTHER INFORMATION: PHOSPHORYLATION
202 <400> SEQUENCE: 9
204 Leu Tyr Arg Ser Pro Ser
205 1 5
207 <210> SEQ ID NO: 10
208 <211> LENGTH: 6
209 <212> TYPE: PRT
210 <213> ORGANISM: Homo sapiens
212 <220> FEATURE:
213 <221> NAME/KEY: MOD_RES
214 <222> LOCATION: (4)..(4)
215 <223> OTHER INFORMATION: PHOSPHORYLATION

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/733,773

DATE: 12/21/2000

TIME: 10:13:40

Input Set : A:\SALK2410.ST25.txt

Output Set: N:\CRF3\12212000\1733773.raw

218 <400> SEQUENCE: 10
220 Gly Ser Ser Ser Pro Val
221 1 5
223 <210> SEQ ID NO: 11
224 <211> LENGTH: 6
225 <212> TYPE: PRT
226 <213> ORGANISM: Homo sapiens
228 <220> FEATURE:
229 <221> NAME/KEY: MOD_RES
230 <222> LOCATION: (4)..(1)
231 <223> OTHER INFORMATION: PHOSPHORYLATION
234 <400> SEQUENCE: 11
236 Pro Pro Ala Thr Pro Pro
237 1 5
239 <210> SEQ ID NO: 12
240 <211> LENGTH: 6
241 <212> TYPE: PRT
242 <213> ORGANISM: Homo sapiens
244 <220> FEATURE:
245 <221> NAME/KEY: MOD_RES
246 <222> LOCATION: (4)..(4)
247 <223> OTHER INFORMATION: PHOSPHORYLATION
250 <400> SEQUENCE: 12
252 Pro Pro Gly Ser Pro Pro
253 1 5
255 <210> SEQ ID NO: 13
256 <211> LENGTH: 6
257 <212> TYPE: PRT
258 <213> ORGANISM: Homo sapiens
260 <220> FEATURE:
261 <221> NAME/KEY: MOD_RES
262 <222> LOCATION: (4)..(4)
263 <223> OTHER INFORMATION: PHOSPHORYLATION
266 <400> SEQUENCE: 13
268 Ser Thr Ser Thr Pro Arg
269 1 5
271 <210> SEQ ID NO: 14
272 <211> LENGTH: 7
273 <212> TYPE: PRT
274 <213> ORGANISM: Homo sapiens
276 <400> SEQUENCE: 14
278 Tyr Ser Pro Thr Ser Pro Ser
279 1 5
281 <210> SEQ ID NO: 15
282 <211> LENGTH: 7
283 <212> TYPE: PRT
284 <213> ORGANISM: Homo sapiens
286 <220> FEATURE:
287 <221> NAME/KEY: MOD_RES

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/733,773

DATE: 12/21/2000

TIME: 19:13:40

Input Set : A:\SALK2410.ST25.txt

Output Set: N:\CRF3\12212000\I733773.raw

```

288 <222> LOCATION: (2)..(2)
289 <223> OTHER INFORMATION: PHOSPHORYLATION
292 <400> SEQUENCE: 15
294 Tyr Ser Pro Thr Ser Pro Ser
295 1 5
297 <210> SEQ ID NO: 16
298 <211> LENGTH: 7
299 <212> TYPE: PRT
300 <213> ORGANISM: Homo sapiens
302 <220> FEATURE:
303 <221> NAME/KEY: MOD_RES
304 <222> LOCATION: (5)..(5)
305 <223> OTHER INFORMATION: PHOSPHORYLATION
308 <400> SEQUENCE: 16
310 Tyr Ser Pro Thr Ser Pro Ser
311 1 5
313 <210> SEQ ID NO: 17
314 <211> LENGTH: 7
315 <212> TYPE: PRT
316 <213> ORGANISM: Homo sapiens
318 <220> FEATURE:
319 <221> NAME/KEY: MOD_RES
320 <222> LOCATION: (2)..(2)
321 <223> OTHER INFORMATION: PHOSPHORYLATION
324 <220> FEATURE:
325 <221> NAME/KEY: MOD_RES
326 <222> LOCATION: (5)..(5)
327 <223> OTHER INFORMATION: PHOSPHORYLATION
330 <400> SEQUENCE: 17
332 Tyr Ser Pro Thr Ser Pro Ser
333 1 5
335 <210> SEQ ID NO: 18
336 <211> LENGTH: 34
337 <212> TYPE: PRT
338 <213> ORGANISM: ARTIFICIAL
340 <220> FEATURE:
341 <223> OTHER INFORMATION: PEPTIDE
343 <400> SEQUENCE: 18
345 Lys Leu Pro Pro Gly Trp Glu Lys Arg Met Ser Arg Ser Ser Glu Arg
346 1 5 10 15
348 Val Tyr Tyr Phe Asn His Ile Thr Asn Ala Ser Glu Trp Glu Arg Pro
349 20 25 30
351 Ser Gly
354 <210> SEQ ID NO: 19
355 <211> LENGTH: 34
356 <212> TYPE: PRT
357 <213> ORGANISM: ARTIFICIAL
359 <220> FEATURE:
360 <223> OTHER INFORMATION: PEPTIDE

```

*Please correct this error in
subsequent sequences.*

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/733,773

DATE: 12/21/2000

TIME: 10:13:41

Input Set : A:\SALK2410.ST25.txt

Output Set: N:\CRF3\12212000\I733773.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 4